

Figure 1a.



Figure 1b.

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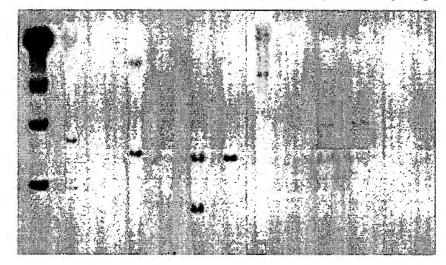


Figure 1c.

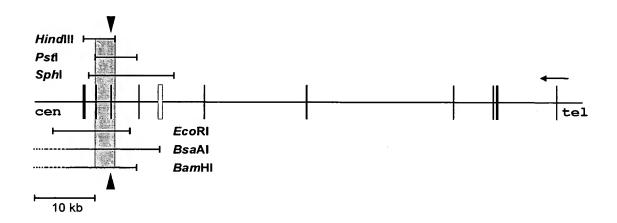


Figure 1d.

hDYXC1 mDYXC1	1 1	MPLOVSDASWOOTKTAMFLSLPLKGVCVRDTDVFCTENYLKVNFPPFLFE MPVRVSEESWOOTPATIFLSLPLKGVCVRDADVFCGESYLKVNFPPFLFE
hDYXC1 mDYXC1	51 51	AFLYAPIDD <mark>ES</mark> SKAKIGNDTINFTLYKKE <mark>AAMWET</mark> LSV <mark>T</mark> GVDKEMMQRIR LFLYAPIDD <mark>GK</mark> SKAKIGNDTINFTLYKKE <mark>PV</mark> IWDSLSV <mark>P</mark> GVDKEMMQRIR
hDYXC1 mDYXC1	101 101	EKSILQAQERAKEATEAKA <mark>A</mark> AKREDORYAL <mark>SV</mark> MMKIEEEERKKIEDMKEN EKSILQAQERAKEATEAKA <mark>V</mark> AKREDORYAL <mark>GE</mark> MMKIEEEERKKIEDIKEN
hDYXC1 mDYXC1	151 151	ERIKATKALEAWKEYORKAĒBOKĶIQREEKLCQKEKOIKEGRKKĪKYKSL ERKKATSELEAWKECOKKADGOKRVORKEKPLE-GKO-ABETKAIKPRGL ^572G->A
hDYXC1 mDYXC1	201 199	TRNLASRNLAPRGRNSENIFTEKLKEDSIPAPRSVGSIKINFTPRVFPTA PRKAPPTRLPTRGRNWENIFPEKLKEDRVPAPRSAGSIQISFTPRVFPTA
hDYXC1 mDYXC1	251 249	LRESQVAEEEEWLHKQAEARRAMNTDIAELCDLKEEEKNPEWLKDKGNKL LRESQVAEEEEWLHKQAEARRAMSTDLPEFFDLKEEEKNPDWLKDKGNKL
hDYXC1 mDYXC1	301 299	FATENYLAATNAYNLAIRLNNKMPLLYLNRAACHLKLKNLHKAIEDSSKA FATENYLAAVDAYNLAIRLNCKIPLLYLNRAACHLKLKNLHKAIEDSSKA ****TPR1********************************
hDYXC1 mDYXC1	351 349	LELLMPPVTDNANARMKAHVRRGTAFCQLELYVEGLQDYEAALKIDPSNK LELLTPPVADNANARMKAHVRRGTAFCQLELYVEGLQDYEAALKIDPANT ******
hDYXC1 mDYXC1	401 399	IVQIDAEKIRNMIQGTELKS MVQNDAEKIRNMIQGTALKSRD 1249G->T^ ^1259C->G

Figure 2a.

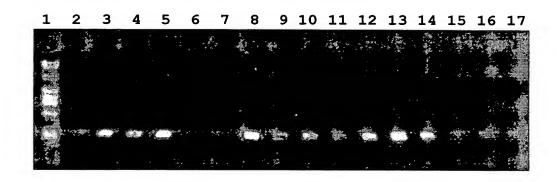


Figure 2b.

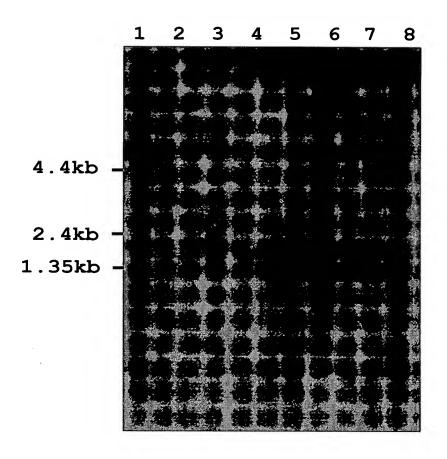


Figure 2c.

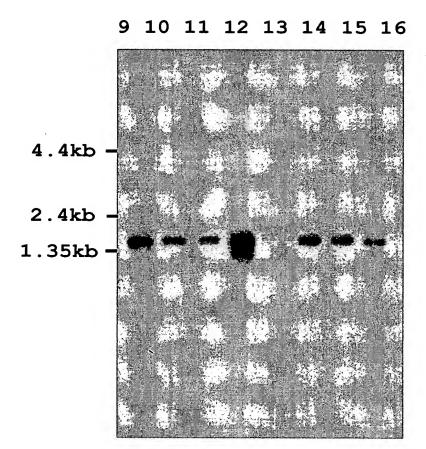


Figure 2d.



Figure 2e.

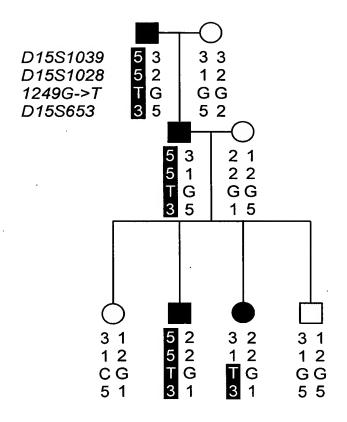


Figure 3.

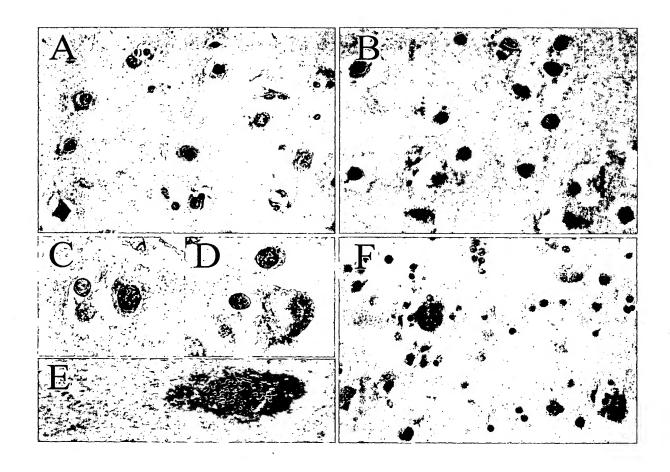


Figure 4

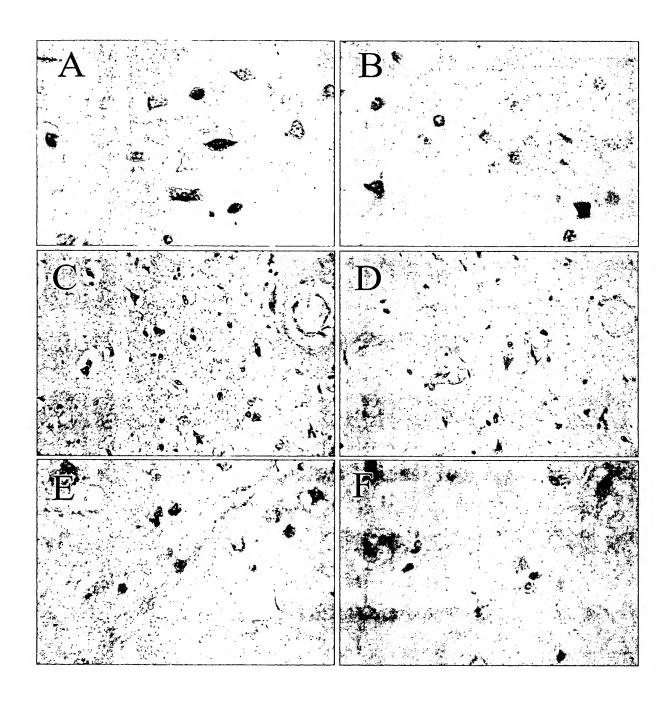


Figure 5